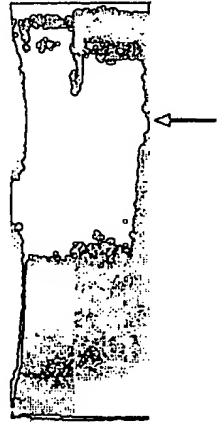




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ :</p> <p>C12N 15/31, C07K 14/22, 16/12, C12Q 1/68, A61K 39/095, G01N 33/50</p>	A2	<p>(11) International Publication Number: WO 99/57280</p> <p>(43) International Publication Date: 11 November 1999 (11.11.99)</p>																								
<p>(21) International Application Number: PCT/US99/09346</p> <p>(22) International Filing Date: 30 April 1999 (30.04.99)</p> <p>(30) Priority Data:</p> <table style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 30%;">60/083,758</td> <td style="width: 40%;">1 May 1998 (01.05.98)</td> <td style="width: 30%;">US</td> </tr> <tr> <td>60/094,869</td> <td>31 July 1998 (31.07.98)</td> <td>US</td> </tr> <tr> <td>60/098,994</td> <td>2 September 1998 (02.09.98)</td> <td>US</td> </tr> <tr> <td>60/099,062</td> <td>2 September 1998 (02.09.98)</td> <td>US</td> </tr> <tr> <td>60/103,749</td> <td>9 October 1998 (09.10.98)</td> <td>US</td> </tr> <tr> <td>60/103,794</td> <td>9 October 1998 (09.10.98)</td> <td>US</td> </tr> <tr> <td>60/103,796</td> <td>9 October 1998 (09.10.98)</td> <td>US</td> </tr> <tr> <td>60/121,528</td> <td>25 February 1999 (25.02.99)</td> <td>US</td> </tr> </table> <p>(71) Applicants (for all designated States except US): CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). THE INSTITUTE FOR GENOMIC RESEARCH [US/US]; 9212 Medical Center Drive, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; Rockville, MD (US). GALEOTTI, Cesira [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). GRANDI, Guido [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). HICKEY, Erin [US/US]; Gaithersburg, MD</p>			60/083,758	1 May 1998 (01.05.98)	US	60/094,869	31 July 1998 (31.07.98)	US	60/098,994	2 September 1998 (02.09.98)	US	60/099,062	2 September 1998 (02.09.98)	US	60/103,749	9 October 1998 (09.10.98)	US	60/103,794	9 October 1998 (09.10.98)	US	60/103,796	9 October 1998 (09.10.98)	US	60/121,528	25 February 1999 (25.02.99)	US
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60/121,528	25 February 1999 (25.02.99)	US																								
<p>(US). MASIGNANI, Vega [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). MORA, Marirosa [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). PETERSEN, Jeremy [US/US]; Arlington, VA (US). PIZZA, Mariagratia [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RAPPUOLI, Rino [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RATTI, Giulio [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCALATO, Enzo [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCARSELLI, Maria [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). TETTELIN, Herve [US/US]; Gaithersburg, MD (US). VENTER, J., Craig [US/US]; Rockville, MD (US).</p> <p>(74) Agent: HARBIN, Alisa, A.; Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA 94662-8097 (US).</p> <p>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p>Published Without international search report and to be republished upon receipt of that report.</p>																										
<p>(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS</p> <p>(57) Abstract</p> <p>The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.</p>																										
<p>919 (46 kDa)</p> <p>A) PURIFICATION</p> <p>M1 919</p> 																										

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DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

a147.seq

```

1   ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCCAAGCG CATGGAAGTG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCAGC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTCTG GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGCGAAACG GCGGACATGG CCGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGCAA CAGGTCGAAA TCCTGCGCGG TCCGTTTACG
451 CTCTTGTACA GCTCGGGCAA TGTGGCGGGG CTGGTTCGATG TTGCGGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGCCTTTGAG CAGCGGCAAT CTGGAAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACTT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTTCGCA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATAACAG GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTTT AACCAACAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCAGTGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACAGCTT
1351 GAAGGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACCTTGAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCCATC AGGAACGCCT
1551 GCCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCAG
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACGACA CCGCGCTACC GCATCGGCGT TTCCGCGGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACC GCCCAC TCATTGCCA AGCCGACCAA AACGCCCTC GCGTTCGGC
2001 TGC GCGCCTC GCGTCCACC TGAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTA TACCGC GTGTTGCGCC AAAACAAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCGGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

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This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

a147.pep

```

1   MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ QVEILRGPVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSQ ELGLRLSSGN LEKLTSGGIN
201 IGLGKNEVLH TEGLYRKSGD YAVPRYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNARIE LRHQPIGRLE
401 GSWG VQYLGQ KSSALSATSE AVKQPMLLDN KVQHYSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYNHNPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLST ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

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1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGTCTAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACACAT TACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GGC CGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCGGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTG GACTACTAC CGCGTGTTCG CCCAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAATA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGCGC GTGAACGTGA
2201 AGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIGVAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWOKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRHD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLQ QKSSALS AIS EAVKQPMLLD
401 NKVQHYSEFFG VEQANWDNFT LEGGVRVEKQ KASIYDKAL IDRENNYHNP
451 LPDLGAHRQT ARSFALSGNW YFTPOHKLST TASHQERLPS TQELYAHGKH
501 VATNTFEVGN KHLNKRSEN IELALGYEGD RWQYNLALYR NRGNYIYAG
551 TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEIFYKP TPRYRIGVSG
601 DYVRGRLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
                                | : | | | | | | | | | | | | | | | | | | | |
g147      MRREAKMAQITLKP IVLSILLINTPLLAQA HETE QSVGLETVSVVGKSR PRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep      TASDKIISG DTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g147      TASDKIISG DTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
              70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g147      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNPPKNA

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601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYR VFAQNKLARY
701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP
751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSRPRATS	SGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGTEQSVGLETVSVVGKSRPRATS	SGLLHTS			
	10	20	30	40	50	60
m147.pep	40	50	60	70	80	90
	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRR	IKVLNHHGET			
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRR	IKVLNHHGET			
	70	80	90	100	110	120
m147.pep	100	110	120	130	140	150
	GDMADFS	PDHAIMVDTALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKI	PEKMPENG	VSG	
a147	GDMADFS	PDHAIMVDSALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKI	PEKMPENG	VSG	
	130	140	150	160	170	180
m147.pep	160	170	180	190	200	210
	ELGLRLSSGNLEKLTSGGINIGLGK	NFVLHTEGLYRKSGDYAVPRY	RNLKRLPD	SHADSQ		
a147	ELGLRLSSGNLEKLTSGGINIGLGK	NFVLHTEGLYRKSGDYAVPRY	RNLKRLPD	SHADSQ		
	190	200	210	220	230	240
m147.pep	220	230	240	250	260	270
	TGSIGLSWVG	EKGFIGVAYS	DRRDQYGLPAHSHEYDDCHAD	IWQKSLINKRYLQ	LYPHL	
a147	TGSIGLSWVG	EKGFIGAAYS	DRRDQYGLPAHSHEYDDCHAD	IWQKSLINKRYLQ	LYPHL	
	250	260	270	280	290	300
m147.pep	280	290	300	310	320	330
	LTEEDIDYDNPGLSCGFHDD	NAHAHNSGRPWIDLRNKRYEL	RAEWKQFPFGFEALRVH			
a147	LTEEDIDYDNPGLSCGFHDD	DAHAHNGKPWIDLRNKRYEL	RAEWKQFPFGFEALRVH			
	310	320	330	340	350	360
m147.pep	340	350	360	370	380	390
	LNRNDYRHDEKAGDAVENFF	NNQTQVARIELRHQPIGRLK	GSWGVQYLQKSSALS	AISE		
a147	LNRNDYRHDEKAGDAVENFF	NNQTQVARIELRHQPIGRLK	GSWGVQYLQKSSALS	SATSE		
	370	380	390	400	410	420
m147.pep	400	410	420	430	440	450
	AVKQPM	LLDNKVQHYSFFGVEQANW	NFTLEGGVRVEKQKASI	QYDKALIDRENYN	HPL	
a147	AVKQPM	LLDNKVQHYSFFGVEQANW	NFTLEGGVRVEKQKASI	RQYDKALIDRENYN	HPL	
	430	440	450	460	470	480
m147.pep	460	470	480	490	500	510
	PDLGAHRQTARSFALS	GNWYFTPOHKLSLTASHQER	LPSTQELYAHGKHVATNT	FEVGNK		
a147	PDLGAHRQTARSFALS	GNWYFTPOHKLSLTASHQER	LPSTQELYAHGKHVATNT	FEVGNK		
	490	500	510	520	530	540
m147.pep	520	530	540	550	560	570
	HLNKERSNNIELALGYEG	DRWQYNLALYRNRF	GNYYAQT	LNDRGRGPKSIEDD	SEM	KLVR
a147	HLNKERSNNIELALGYEG	DRWQYNLALYRNRF	GNYYAQT	LNDRGRGPKSIEDD	SEM	KLVR

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	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFIAQDDQ					
a147	YNQSGADFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPLIAQADQ					
	610	620	630	640	650	660
m147.pep	640	650	660	670	680	690
	NAPRVPAARLGFHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCGA
51  AgctATgagt  gtcggcgCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gGCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCGT  CCTGCAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTGATTTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAaCGtcg  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTAcg  cgcTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGa  tgccgTCAAA  CCCGGTTTCGC
401 GCGTCCTGCT  GGTGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgcgcgcgC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

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This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

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g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGSRVLLVDD  LVATGGTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCGA
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCGT  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTGATTTA  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGA  TGCCGTCAAA  CTCGGTTTCGC
401 GCGTGCTGCT  GGTGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGAATGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGCAAGCG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENYI NQPLPDLGAH RQTARSFALS GNWYFTP HHK
501 LSLTASHQER LPSTQELYAH GKHVATNTE VGNKHLNKER SNNIELALGY
551 EGDRAWQYNLA AYRNRFNGYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPYKRPFFIA
651 QADQNAIPRI AARLGFHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGCG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGCGATTTT TCGCCCGATC ACGCCATTAT GGATAGATAC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTTGCCGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAA GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGGAAAA ACTCACGTCC GCGCGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCGTGCC CGACAGCCAC GCCGATTGCG
701 AAACGGGCGA CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAACGCTA TTTACAGCTT TATCCGCACC TGTTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAATC CCGTGCCGAA TGGAAGCAAC CGTTCCCGCG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCCGCA CCAACCCATA GGTCTGTCTG AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTTAA
1251 ACAACCGATG CTGCTTGACA ACAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AACTGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAACCTACTA AACCAACCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTTC GGCACCTGGT ATTTACGCGC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACAG TCGCCACCAA CACCTTGAA GTCCGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACGCGA ACCGCTTCGG
1701 TAACTACATT TACGCCCCAA CCTTAAACGA CGGACGCGGC CCCAATCCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGCGGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCGC ACTATGTACG AGGCGCTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCTACG GCAACCGTCC TTTTATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCCG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTTCTC TCTGATACG CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGO
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTS GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTSGISL SWVGEKGFIF
251 VAYSRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPPGFEEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTN ARIELRHQPI GRLKGSWGVO
401 YLQKSSALS AISEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENYI NHPLPDLGAH RQTARSFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTE VGNKHLNKER SNNIELALGY

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g149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGTCAG	CGTCGTCGGC	AAAAGCCGTC	CGCGCGCGAC	TTCGGGGCTG
151	CTGCACACTT	CGACCGCCTC	CGACAAAAATC	ATCTCCGGCG	AGTCTTTGCG
201	CCAAAAAGAG	GTCAACTTGG	GCGACGCTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGCG	GGCGCATCCG	CTCCCGTTAT	TCGCGGTCAA
301	ACGGGCAGAC	GGATTAAGT	ATTGAACAT	CACGGCGAAA	CGGGCGATAT
351	GGCGGACTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTCGG
401	AACAGTTTGA	AATCTTCGCC	GGGCGCGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTGA	TGTTGCCGAT	GGAAAAATCC	CGCAAAAAAT
501	GCCTGAAAAC	GGCGTATCGG	GCGAagccgG	ATTGCGTTTG	AGCAGCGGCA
551	ATTTAGAAAA	ACTGACATCC	GCAGGCATCA	ATATCGGACT	GGGCAAAAAAC
601	TTCGTGCTGC	ATACCGAAGG	CTTGTCACGC	AAATCGGGCG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AAGCGCTGCC	CGACAGCCAT	GCCGATTTCG
701	AAACGGGGCG	CATCGGGGCTG	TC TTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	GCAGCATACA	CGCAGCGTCG	CGACCGCTAC	GGCCTGCCTG	CCCACAGCCA
801	CGAATACGAT	GATTGCCACG	CGCATCTATC	CTGGCAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTGACGCTT	TATCCGCATC	TGTTGACCGA	AGAAGACATA
901	GATTACGACA	ATCCGGGCTT	GAGCTCGCGC	TTCACGACG	CGCAGCGGTG
951	ACACGCACAC	ACCCACAACG	GCAAAACGTG	GATAGACTCT	GCGAACAAAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTGCGCGTAC	ATCTGAACCG	CAATGACTAC	CACACACGAC	AAAAAGCAGG
1101	CGATGCACTA	GAAAACTTCT	TCAACAAACA	AACACACAGC	GCCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTCCG	GCCATTCCCC	AAACCGTCCA
1251	ACAACCGATG	TGATTGACA	ACAATGTCCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTCACGC	TGGAAGGCGG	GTACGCGCTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGGTACGAC	AAAGCATTTA	TTGATTCGAA
1401	AAACTACTAC	AACCAAGCCC	TGCCGACCTT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTCGTT	CGCACTTTTG	GCGAAC TTGGT	ATTTCACGCC	ACACCAACAA
1501	CTCAGCCTGA	CCGCCTCCCA	TCAGGAACCA	CTGCCGTCAA	CGCAAGAACT
1551	GTACGCGCAC	GGAAGCAGC	TCGCCACCAA	CACCTTTGAA	GTCGCGCAAC
1601	AACACCTCAA	CAAGAGCGTT	TCCAACATA	TCGAACTCGC	GCTGGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCCCCAA	AGCTAAACAG	CGGACGCGCG	CCCAATTCCT
1751	TCGAAGACGA	CACGGAATAG	CAACTCGTGC	GCTACAACCA	ATCCGGTGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCACTCGT	GTTTCCGGCG	ACTATGTGAC	AGGCCGCTGT	AAAAACCTGC
1901	CGTCCCTACC	CGGCAGGGAA	GATCCCTACG	GCAACGCTCC	CTTCACTCGA
1951	CAAGCCGACG	AAAACGCCCC	CCGCAATTCCG	GCTGCGCGCG	TCCGCTTCCA
2001	CCTGAAAAAC	TCGCTAACCG	ACCGTATCGA	TGCCAAATTG	GACTACTACC
2051	CGGTGTTCCG	CCAAACACAA	CTCGCCCGCT	ACGAAATCGG	TACGCCCCGA
2101	CACCATATGC	TCAACCTCGG	TGCAAACTAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGGAAAT	TGGTAGCTCA	AAGCGATACG	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCCCACG	CAGCTTCTCT	TCTGTATACG	CGCAAATGGG	CCGCGAGCTT
2251	ACCGGCGGGC	TAAACGTGAA	GTTTTTAA		

g149-1.pep

1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRLQA	VNLGDALDGV	PGIHASQYGG	GASAPVIRGQ
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMVDV	ALSQQVEILR	GPVTLLYSSG
151	NVAGLVVDAD	GKI PEKMPEN	GSVGEAGRLR	SSGNLEKLTS	AGNIGLGNK
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSQTSGISL	SWVGKEGFIG
251	AAYSRRDRY	GLPAHSHEYD	DCHADIWQK	SLINKRYLQL	YPHLLTEDDI
301	YDYNPGLSCG	FHDGGAHAH	THNGKEPIDL	RNKRYELRAE	WKOPFPGEFA

551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNOSGA
 601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPPIA
 651 QDDQNAAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
 751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQA	HETE	QSV	DL	ETVSVVGKSRPRATSGLLHTSTASDKI	
g149-1	MAQITLKPIVLSILLINTPLLAQA	HETE	QSV	GL	ETVSVVGKSRPRATSGLLHTSTASDKI	
	10	20	30	40	50	60
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
g149-1	SPDHAIMVDTALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
	130	140	150	160	170	180
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVL	HTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL				
g149-1	SSGNLEKLTSGGINIGLGKNFVL	HTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL				
	190	200	210	220	230	240
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVAYSDDRRDQYGL	PAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI				
g149-1	SWVGEKGFIVAYSDDRRDQYGL	PAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI				
	250	260	270	280	290	300
	310	320	330	340	350	360
m149-1.pep	DYDNPGLSCGFHDDNAHAHTH	SGRPWIDLNRNKRYELRAEWKQFPFGFEALRVHLNRNDY				
g149-1	DYDNPGLSCGFHDDNAHAHTH	SGRPWIDLNRNKRYELRAEWKQFPFGFEALRVHLNRNDY				
	310	320	330	340	350	360
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTQNA	RIELRHQPIGRLKGSWGVQYLQKSSALSASEAVQQPM				
g149-1	HHDEKAGDAVENFFNNKTHNA	RIELRHQPIGRLKGSWGVQYLQKSSALSAPETVQQPM				
	370	380	390	400	410	420
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSFFGVEQANWDN	FTLEGGVRVEKQKASIQYDKALIDRENYYNHPLPDLGAH				
g149-1	LIDNNVRHYSFFGVEQANWDN	FTLEGGVRVEKQKASIRYDKALIDRENYYNQPLPDLGAH				
	430	440	450	460	470	480
	490	500	510	520	530	540
m149-1.pep	RQTARSFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
g149-1	RQTARSFALSGNWFYTPHHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
	490	500	510	520	530	540
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLA	LYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNOSGA			
g149-1	SNNIELALGYEGDRWQYNLA	LYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNOSGA			
	550	560	570	580	590	600
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGREGDAYGNRPPIAQDDQNAAPRVP				
g149-1	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGREDPYGKRPFIAQADQNAAPRIP				
	610	620	630	640	650	660

a149-1.seq

a149-1.pcp

1	MAQTTLKPIV	LSILLINTPL	LSQAHGTEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLTRQA	VNLGDALDGV	PGIHASQYGG	GASAPVIRSG
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMVDS	ALSQQVEILR	GPVTLTRYSG
151	NVAGLVVDAD	GKIPKMPEN	GVSGELGLRL	SSGNLEKLTG	GGNIGLGNK
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSGTGRYGL	SWUGEKFTIG
251	AAYSDDRRDQY	GLPAHSHEYD	DCHADIWIQK	SITNGKISLQ	YPHLLTEEDI
301	DYDNPGLSCG	FHDDDDAHAH	AHNGKPWIDL	RNKRYELRAE	WQOFFPGFEA

351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DAYGNRPLIA
651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVLDLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPGLSGCFHDDDDAHAHAHNGKPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY					
m149-1	DYDNPGLSGCFHDDDDAHAHAHNGKPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVOYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVOYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPPLDLGAH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARFALS GNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARFALS GNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

a149-1.pep	DFYGAEGEYIFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNA PRVP
m149-1	DFYGAEGEYIFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNA PRVP
	610 620 630 640 650 660
a149-1.pep	AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
m149-1	AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
	670 680 690 700 710 720
a149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
m149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
	730 740 750 759

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

```

1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTGCGC GTTGCTCCG
251 CACTGTTATC CCATTCGAA CTCACGAAA ACACCCCGC CTTTGTCAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAATTCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCCGCCT GTATTGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTTC GAACACGAAG
551 GGCGCGCCAG GGCGGGCGGC GCATCGGGT TCTTTGCCGA CCGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGCAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCG GGCATTGCGA CGAAGACGGC
1051 GCAGAAGGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

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1  ..YCKADPFPA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTLP VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQORAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDF LHRDYFAWSR DQEEKIYVQD
301 KIREQAEGW QWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDEDE
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

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1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCACGCA
51  GCTCCTGTCT GGGCTGGACG CGGCACAATG GGCGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTACG
151 ACGGCATTGC CGCGGCGAGA ACCTTTTCC GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCCG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGGCGAACG CCGCCTGCTG CTGGTTACCT CCACCCAAGG
351 CGAAGGCGAA CCGCGGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAACTCC AATTGCGCGT ACTGGGTTTG

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